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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/927,395

DATE: 11/21/2001

TIME: 12:26:52

Input Set : N:\Crf3\RULE60\09927395.txt

Output Set: N:\CRF3\11212001\I927395.raw

3 <110> APPLICANT: LIVSHITS, VITALY ARKADIEVICH  
4 ZAKATAEVA, NATALYA PAVLOVNA  
5 ALCOSHIN, VLADIMIR VENYAMIOVICH  
6 BELAREOVA, ALL VALENTINOVNA  
7 TOKHMAKOVA, IRINA LVOVNA  
9 <120> TITLE OF INVENTION: DNA CODING FOR PROTEIN WHICH CONFERS ON BACTERIUM  
10 ESCHERICHIA COLI RESISTANCE TO L0-HOMOSERINE AND METHOD  
11 FOR PRODUCING L-AMINO ACIDS  
13 <130> FILE REFERENCE: 0010-1039-0  
15 <140> CURRENT APPLICATION NUMBER: 09/927,395  
16 <141> CURRENT FILING DATE: 2001-08-13  
18 <150> PRIOR APPLICATION NUMBER: 09/396,357  
19 <151> PRIOR FILING DATE: 1999-09-15  
21 <150> PRIOR APPLICATION NUMBER: RU98118425  
22 <151> PRIOR FILING DATE: 1998-10-13  
24 <160> NUMBER OF SEQ ID NOS: (2)  
26 <170> SOFTWARE: PatentIn Ver 2.1  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 1200  
30 <212> TYPE: DNA  
31 <213> ORGANISM: Escherichia coli  
33 <220> FEATURE:  
34 <221> NAME/KEY: CDS  
35 <222> LOCATION: (557)..(1171)  
37 <400> SEQUENCE: 1  
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42 cgattaacat gcccgagatg cggatcggct aacaggcgac cggaacgtcc ctgcccgcg 180  
44 tggctgatga ttaagacatc aaaccccaaa tggaacaggt cataggccag ttccgcatat 240  
46 tttaacgtagc tctcaatacg ccccgggcag atgactacca cccggtcatg gtgctgtgcg 300  
48 cgaaaacgga caaagcgcac cggaatgtca tccacaccag taaactctgc ttcacacgc 360  
50 tgacgccaga aatcagtcag cgggccatg gtaaaagcag caaacgcgtt ttctcttgg 420  
52 tcccagtcct tttgctgctg aaacatcggg taatctgcct cttaaaccac gtaaaatcgt 480  
54 ttttttttagc gtgctgaca caacgtgctg acagtagcgt attgtggcac aaaaatagac 540  
56 acaccgggag ttcacatc atg acc tta gaa tgg tgg ttt gcc tac ctg ctg aca 592  
57 Met Thr Leu Glu Trp Trp Phe Ala Tyr Leu Leu Thr  
58 1 5 10  
60 tcg atc att tta acg ctg tcg cca ggc tct ggt gca atc aac act atg 640  
61 Ser Ile Ile Leu Thr Leu Ser Pro Gly Ser Gly Ala Ile Asn Thr Met  
62 15 20 25  
64 acc acc tcg ctc aac cac ggt tat ccg gcc ggt ggc gtc tat tgc tgg 688  
65 Thr Thr Ser Leu Asn His Gly Tyr Pro Ala Gly Gly Val Tyr Cys Trp  
66 30 35 40  
68 gct tca gac cgg act ggc gat tca tat tgt gct ggt tgg cgt ggg gtt 736  
69 Ala Ser Asp Arg Thr Gly Asp Ser Tyr Cys Ala Gly Trp Arg Gly Val  
70 45 50 55 60  
72 ggg acg cta ttt tcc cgc tca gtg att gcg ttt gaa gtg ttg aag tgg 784

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73 Gly Thr Leu Phe Ser Arg Ser Val Ile Ala Phe Glu Val Leu Lys Trp
74          65          70          75
76 gca ggc gcg gct tac ttg att tgg ctg gga atc cag cag tgg cgc gcc      832
77 Ala Gly Ala Ala Tyr Leu Ile Trp Leu Gly Ile Gln Gln Trp Arg Ala
78          80          85          90
80 gct ggt gca att gac ctt aaa tcg ctg gcc tct act caa tcg cgt cga      880
81 Ala Gly Ala Ile Asp Leu Lys Ser Leu Ala Ser Thr Gln Ser Arg Arg
82          95          100          105
84 cat ttg ttc cag cgc gca gtt ttt gtg aat ctc acc aat ccc aaa agt      928
85 His Leu Phe Gln Arg Ala Val Phe Val Asn Leu Thr Asn Pro Lys Ser
86          110          115          120
88 att gtg ttt ctg gcg gcg cta ttt ccg caa ttc atc atg ccg caa cag      976
89 Ile Val Phe Leu Ala Ala Leu Phe Pro Gln Phe Ile Met Pro Gln Gln
90 125          130          135          140
92 ccg caa ctg atg cag tat atc gtg ctc ggc gtc acc act att gtg gtc      1024
93 Pro Gln Leu Met Gln Tyr Ile Val Leu Gly Val Thr Thr Ile Val Val
94          145          150          155
96 gat att att gtg atg atc ggt tac gcc acc ctt gct caa cgg att gct      1072
97 Asp Ile Ile Val Met Ile Gly Tyr Ala Thr Leu Ala Gln Arg Ile Ala
98          160          165          170
100 cta tgg att aaa gga cca aag cag atg aag gcg ctg aat aag att ttc      1120
101 Leu Trp Ile Lys Gly Pro Lys Gln Met Lys Ala Leu Asn Lys Ile Phe
102          175          180          185
104 ggc tcg ttg ttt atg ctg gtg gga gcg ctg tta gca tcg gcg agg cat      1168
105 Gly Ser Leu Phe Met Leu Val Gly Ala Leu Leu Ala Ser Ala Arg His
106          190          195          200
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109 Ala
110 205
113 <210> SEQ ID NO: 2
114 <211> LENGTH: 205
115 <212> TYPE: PRT
116 <213> ORGANISM: Escherichia coli
118 <400> SEQUENCE: 2
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123          20          25          30
125 Asn His Gly Tyr Pro Ala Gly Gly Val Tyr Cys Trp Ala Ser Asp Arg
126          35          40          45
128 Thr Gly Asp Ser Tyr Cys Ala Gly Trp Arg Gly Val Gly Thr Leu Phe
129          50          55          60
131 Ser Arg Ser Val Ile Ala Phe Glu Val Leu Lys Trp Ala Gly Ala Ala
132 65          70          75          80
134 Tyr Leu Ile Trp Leu Gly Ile Gln Gln Trp Arg Ala Ala Gly Ala Ile
135          85          90          95
137 Asp Leu Lys Ser Leu Ala Ser Thr Gln Ser Arg Arg His Leu Phe Gln
138          100          105          110
140 Arg Ala Val Phe Val Asn Leu Thr Asn Pro Lys Ser Ile Val Phe Leu

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```

141          115          120          125
143 Ala Ala Leu Phe Pro Gln Phe Ile Met Pro Gln Gln Pro Gln Leu Met
144          130          135          140
146 Gln Tyr Ile Val Leu Gly Val Thr Thr Ile Val Val Asp Ile Ile Val
147 145          150          155          160
149 Met Ile Gly Tyr Ala Thr Leu Ala Gln Arg Ile Ala Leu Trp Ile Lys
150          165          170          175
152 Gly Pro Lys Gln Met Lys Ala Leu Asn Lys Ile Phe Gly Ser Leu Phe
153          180          185          190
155 Met Leu Val Gly Ala Leu Leu Ala Ser Ala Arg His Ala
156          195          200          205

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VERIFICATION SUMMARY

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